Amendments to the Specification:

Please amend the specification as follows.

Please replace paragraph starting at page 2, line 22, with the following rewritten paragraph:

A method to synthesize a full length cDNA is known to those skilled in the art. For example, the oligo-capping method (Maruyama K. and Sugano S. (1994) Gene 138: 171-174; Suzuki Y. et al. (1997) Gene 20: 149-156) enables to synthesize a library enriched with full length cDNA, in principle. Once the synthesized cDNA is cloned and the nucleotide sequence is determined, it is possible to estimate whether the cDNA is a full length cDNA clone or not by methods such as the ATGpr (Salamov A.A., Nishikawa T., and Swindells M.B. (1998) Bioinformatics 14: 384-390~~; http://www.hri.co.jp/atgpr/~~). However, synthesis efficiency needs to be improved, although it is possible to obtain full length cDNA in a certain probability by combining known methods. It is still difficult to clone a full length cDNA of mRNA that is expressed at very low frequency.

Please replace paragraph starting at page 3, line 14, with the following rewritten paragraph:

Furthermore, the inventors have analyzed the nucleotide sequence of the full length cDNA clones obtained by the method, and deduced the amino acid sequence encoded by the nucleotide sequence. Then, the inventors have performed the BLAST search (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) J. Mol. Biol. 215: 403-410; Gish W., and States D.J. (1993) Nature Genet. 3: 266-272~~; http://www.ncbi.nlm.nih.gov/BLAST/~~) of the GenBank ~~(http://www.ncbi.nlm.nih.gov/Web/GenBank/index.html)~~ and SwissProt ~~(http://www.ebi.ac.uk/ebi_docs/swissprot_db/swisshome.html)~~ using the deduced amino acid sequence to accomplish the present invention.

Please replace paragraph starting at page 7, line 37, with the following rewritten paragraph:

Since any protein encoded by the cDNA clone of the invention contains its full length amino acid sequence, it is possible to analyze its biological activity by expressing it as a recombinant protein utilizing an appropriate expression system, or by using a specific antibody against it. If the protein is associated with diseases, a specific antibody obtained by using the expressed protein can be utilized to examine the relationship between the expression level or activity of the protein and a particular disease. Alternatively, it is possible to analyze the relationship between the protein and disease by using the Online Mendelian Inheritance in Man (OMIM) (~~http://www.ncbi.nlm.nih.gov/Omim/~~), the database of human genes and diseases. Proteins associated with diseases are useful in drug development since they can be utilized as a diagnostic marker, a drug that regulates the level of their expression and activity, or a target of gene therapy. Especially, the protein associated with transcription or signal transduction is extremely useful in the medicinal industry because the associations of such a protein with diseases have been reported in "Transcription factor research 1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit. (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene medical" (1999) Vol.3, No.2.

Please replace paragraph starting at page 12, line 36, with the following rewritten paragraph:

The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res.25:3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. ~~See http://www.ncbi.nlm.nih.gov.~~